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Unravelling plant-biotic/abiotic stress using computational biology and bioinformatics tools.

Monday, 1 December 2025 14:10 (20 minutes)

Major discoveries in molecular biology, along with advances in bioinformatics technologies, have resulted in an exponential increase in the biological data supplied by the scientific community over the past few decades. Genomics, transcriptomics, proteomics, and metabolomics are four of the techniques that have impacted studies in plant-biotic/abiotic stress. When used singly, each of these procedures can generate a massive amount of data, however, when utilized together, they have the potential to fully dissect a system at the transcriptional and translational levels.

Our research focuses on understanding interactions between plants and biotic/abiotic factors for resistance/tolerance breeding purposes in crops such as cassava, wheat, sweetpotato and common bean, among others. The use computational biology and bioinformatics can enhance an understanding of plant-stress responses and aid in the development of stress-resistant/tolerant plants. These advancements can boost yields, increase agricultural productivity, and enhance global food security. Access to computing resources such as the CHPC is needed to achieve these results, hence, the presentation will showcase studies that were achieved using these tools, including the ongoing and future studies.

Presenting Author

Email

Student or Postdoc?

CHPC User

CHPC Research Programme

Workshop Duration

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Session Classification: HPC Applications